

**REMARKS**

Enclosed herewith is a hard copy and computer readable copy of the sequence listing along with a copy of the Notice to Comply. The required statements regarding the sequence listing are also enclosed herewith.

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

Should additional fees be necessary in connection with the filing of this paper, the Commissioner is hereby authorized to charge Deposit Account No. 50-0320 for any such fees.

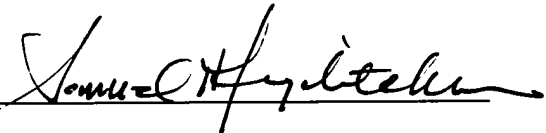
**CONCLUSION**

It is respectfully submitted that the application now complies with all requirements set forth in the Notice, including the requirements for computer readable disclosure of the biological sequences under 37 C.F.R. §1.821-1.825. Consequently, reconsideration and withdrawal of the Notice to Comply is respectfully requested.

Respectfully submitted,

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**MARKED UP VERSION ATTACHED TO AMENDMENT IN**

**SERIAL NO. 09/732,348**

**Marked up version of the paragraph starting at page 8, line 3, is below:**

Figure 9 depicts expression of 1XBSGFP and 1XBMRFP in onion peels. The oligonucleotides are shown in SEQ ID NOS 30 & 31, respectively.

**Marked up version of the paragraph starting at page 11, line 8, to page 12, line 2, is below:**

In a preferred aspect of the present invention, zinc finger nucleic acid binding motifs may be represented as motifs having the following primary structure:

(B)  $X^a$  **C**  $X_{2-4}$  **C**  $X_{2-3}$   $F X^c X X X L X X H X X X^b H$  – linker (SEQ ID NO: 22)

wherein X (including  $X^a$ ,  $X^b$  and  $X^c$ ) is any amino acid.  $X_{2-4}$  and  $X_{2-3}$  refer to the presence of 2 or 4, or 2 or 3, amino acids, respectively, and  $X X X X L X X H X X$  between  $X^c$  and  $X^b$  are designated position -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9. The Cys and His residues, which together co-ordinate the zinc metal atom, are marked in bold text and are usually invariant, as is the Leu residue at position +4 in the  $\alpha$ -helix.

**Marked up version of the paragraph starting at page 13, line 3, is below:**

Preferably, the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24).

**Marked up version of the paragraph starting at page 15, line 5-9, is below:**

Consensus zinc finger structures may be prepared by comparing the sequences of known zinc fingers, irrespective of whether their binding domain is known. Preferably, the consensus structure is selected from the group consisting of the consensus structure P Y K

C P E C G K S F S Q K S D L V K H Q R T H T G (SEQ ID NO: 25), and the consensus structure P Y K C S E C G K A F S Q K S N L T R H Q R I H T G E K P (SEQ ID NO: 26).

**Marked up version of the paragraph starting at page 15, lines 10-15, is below:**

The consensuses are derived from the consensus provided by Krizek *et al.*, (1991) J. Am. Chem. Soc. 113: 4518-4523 and from Jacobs, (1993) PhD thesis, University of Cambridge, UK. In both cases, the linker sequences described above for joining two zinc finger motifs together, namely TGEK (SEQ ID NO: 23) or TGEKP (SEQ ID NO: 24) can be formed on the ends of the consensus. Thus, a P may be removed where necessary, or, in the case of the consensus terminating T G, E K (P) can be added.

**Marked up version of the paragraph starting at page 19, lines 5-6, is below:**

A "leader" peptide may be added to the N-terminal finger. Preferably, the leader peptide is MAEEKP (SEQ ID NO: 27).

**Marked up version of the paragraph starting at page 52, lines 16-22, is below:**

The DNA binding site for the TFIIIAZif protein contains the DNA recognition sites for zinc fingers 1-3 of TFIIIA and the three zinc fingers of Zif 268. These are the DNA sequences GGATGGGAGAC (SEQ ID NO: 32) and GCGTGGGCGT (SEQ ID NO: 33), respectively. The six base pair sequence GTACCT in Sequence ID NO:3 is a spacer region of DNA that separates the two binding sites and the nucleotide composition of the DNA spacer appears to have no effect on binding of the protein. Therefore, this or other structured linkers could be used with other DNA spacers of different length and sequence.

**Marked up version of the paragraph starting at page 53, lines 1-3, is below:**

The amino acid sequence of zinc Finger 4 of TFIIIA, including the flanking sequences as used in the composite protein of the invention, is

NIKICVYVCHFENCGKAFKKHNQLK VHQFSHTQQLP (SEQ ID NO: 28).

**Marked up version of the paragraph starting at page 53, lines 4-6, is b low:**

The nucleotide Sequence of Zinc Finger 4 of TFIIIA, including the flanking sequences, is  
AACATCAAGATCTGCGTCTATGTGTGCCATTTTGAGAACTGTGGCAAAGCATTCAAGAA  
ACACAATCAATTAAAGGTTTCATCAGTTCAGTCACACACAGCAGCTGCCG (SEQ ID NO: 29).

**In the Claims:**

Please amend the claims as follows:

26. (Amended) The plant host cell or transgenic plant of claim 25 wherein the zinc finger structures have a binding motif represented by:

$X^a \text{C} X_{2-4} \text{C} X_{2-3} F X^c X X X X L X X H X X X^b H$  – linker (SEQ ID NO: 22)  
wherein each of X,  $X^a$ ,  $X^b$ ,  $X^c$  is any amino acid, the numbers in subscript indicate possible numbers of residues, and  $X X X X L X X H X X$  between  $X^c$  and  $X^b$  are designated positions -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9.

27. (Amended) The plant host cell or transgenic plant of claim 26 wherein  $X^a$  is E, K, T, S, Q, V, A or P,  $X^b$  is T or I,  $X^c$  is S or T,  $X_{2-4}$  is two amino acids, with the first of which being S, E, K, T, P, or R, and the second amino acid being E, and the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24), and position 9 is Arg or Lys, and positions 1, 5, and 8 are hydrophobic amino acids and not Phe, Trp or Tyr.

29. (Amended) The plant host cell or transgenic plant of claim 26 wherein there is an N-terminal zinc finger having a leader peptide MAEEKP (SEQ ID NO: 27) added thereto.

53. (Amended) The method of claim 52 wherein the zinc finger structures have a binding motif represented by:

$X^a \text{C} X_{2-4} \text{C} X_{2-3} F X^c X X X X L X X H X X X^b H$  – linker (SEQ ID NO: 22)  
wherein each of X,  $X^a$ ,  $X^b$ ,  $X^c$  is any amino acid, the numbers in subscript indicated possible numbers of residues, and  $X X X X L X X H X X$  between  $X^c$  and  $X^b$  are designated positions -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9.

54. (Amended) The method of claim 53 wherein  $X^a$  is E, K, T, S, Q, V, A or P,  $X^b$  is T or I,  $X^c$  is S or T,  $X_{2-4}$  is two amino acids, with the first of which being S, E, K, T, P, or R, and the second amino acid being E, and the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24), and position 9 is Arg or Lys, and positions 1, 5, and 8 are hydrophobic amino acids and not Phe, Trp or Tyr.

56. (Amended) The method of claim 53 wherein there is an N-terminal zinc finger having a leader peptide MAEEKP (SEQ ID NO: 27) added thereto.